

Access DB# 135705

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 10/24/04
 Art Unit: 1635 Phone Number 302-0765 Serial Number: 091471-067
 Mail Box and Bldg/Room Location: 2d 28 Results Format Preferred (circle): PAPER DISK E-MAIL
2C18

If more than one search is submitted, please prioritize searches in order of need. MEJ

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.
 Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or
 utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if
 known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: NA LaddersInventors (please provide full names): J/u et al.Earliest Priority Filing Date: 3-26-98

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the
 appropriate serial number.

Please search Seq IDs 1-4. 34
Zara 067

- with following arrangement:

NA-10- (1) seq 1 + 1 or seq 1 + complement of 1
 NA-10- (2) seq 2 + 2 or seq 2 + complement of 2
 NA-10- (3) seq 3 + 3 or seq 3 + complement of 3
 NA-10- (4) seq 4 + 4 or seq 4 + complement of 4

MEJ

For references & regular
 job bases please

EXACT IDENTITY needed. MEJ

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>P. Schaefer</u>	NA Sequence (#) <u>8</u>	STN _____
Searcher Phone #: <u>272-2526</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>Rensselaer EOI ASI</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: <u>10/28</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>15</u>	Fulltext _____	Sequence Systems <u>Compuser Ig</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>37</u>	Other _____	Other (specify) _____

File 159:Cancerlit 1975-2002/Oct
(c) format only 2002 Dialog Corporation
File 164:Allied & Complementary Medicine 1984-2004/Dec
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File 444:New England Journal of Med. 1985-2004/Nov W4
(c) 2004 Mass. Med. Soc.
File 467:ExtraMED(tm) 2000/Dec
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Set	Items	Description
S1	0	NUCLEIC ACID LADDER?
S2	560	DNA LADDER?
S3	0	S2 (S) RESTRICTION
S4	27	S2 AND ENDONUCLEASE?
S5	25	RD (unique items)

>>>KWIC option is not available in file(s): 399

5/3,K/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2004 BIOSIS. All rts. reserv.

0014837034 BIOSIS NO.: 200400204667

Mechanism of enhanced vulnerability to NMDA toxicity in secondary traumatic neuronal injury.

AUTHOR: Arundine M (Reprint); Chopra G K; Wrong A (Reprint); Lei S (Reprint); Aarts M M; Wallace M; Macdonald J F (Reprint); Tymianski M (Reprint)

AUTHOR ADDRESS: Physiology, Univ. of Toronto, Toronto Western Res. Inst., Toronto, ON, Canada**Canada

JOURNAL: Society for Neuroscience Abstract Viewer and Itinerary Planner
2003 pAbstract No. 743.2 2003 2003

MEDIUM: e-file

CONFERENCE/MEETING: 33rd Annual Meeting of the Society of Neuroscience New Orleans, LA, USA November 08-12, 2003; 20031108

SPONSOR: Society of Neuroscience

DOCUMENT TYPE: Meeting; Meeting Abstract

RECORD TYPE: Abstract

LANGUAGE: English

...ABSTRACT: a pan caspase inhibitor z-vad-FMK did not attenuate vulnerability to NMDA, suggesting against a classical apoptotic mechanism. Moreover, apoptosis-inducing factor (AIF) and *endonuclease*-G did not translocate into the nucleus, suggesting against caspase independent apoptotic mechanisms. Stretched neurons exhibited a rapid production of reactive oxygen and nitrogen species...

DESCRIPTORS:

METHODS & EQUIPMENT: *DNA laddering*...

5/3,K/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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0014301368 BIOSIS NO.: 200300260012

Effect of hypoxia on DNA fragmentation in the cerebral cortex of the guinea pig fetus at different gestational ages.

AUTHOR: Abedin Naheed (Reprint); Ashraf Oazi M (Reprint); Randis Tara (Reprint); Mishra Om P (Reprint); Delivoria-Papadopoulos Maria (Reprint)

AUTHOR ADDRESS: Dept. of Pediatrics, Drexel University and St.

Christopher's Hospital for Children, Philadelphia, PA, USA**USA

JOURNAL: Pediatric Research 53 (4 Part 2): p48A-49A April 2003 2003

MEDIUM: print

CONFERENCE/MEETING: Annual Meeting of the Pediatric Academic Societies' Seattle, WA, USA May 03-06, 2003; 20030503

SPONSOR: Pediatric Academic Societies

ISSN: 0031-3998 (ISSN print)

DOCUMENT TYPE: Meeting; Meeting Abstract

File 5: Biosis Previews(R) 1969-2004/Nov W3
(c) 2004 BIOSIS

File 6: NTIS 1964-2004/Nov W4
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File 99: Wilson Appl. Sci & Tech Abs 1983-2004/Oct
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(c) 2004 Contains copyrighted material

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(c) 2004 Royal Soc Chemistry

File 393: Beilstein Abstracts July 2004
(c) 2004 Beilstein GmbH

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(c) 2004 ProQuest Info&Learning

File 48: SPORTDiscus 1962-2004/Dec
(c) 2004 Sport Information Resource Centre

File 91: MANTIS(TM) 1880-2004/Nov
2001 (c) Action Potential

File 149: TGG Health&Wellness DB(SM) 1976-2004/Nov W1
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 11:49:55 ; Search time 710.125 Seconds
(without alignments)
1331.870 Million cell updates/sec

Title: SEQ4-C4
Perfect score: 20
Sequence: 1 atcatgcagatcgcagat 20

Scoring table: OLIGO_NJC
Gapop 60.0, Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

GenBank1:
1: gb_ba:*
2: gb_ptg:*
3: gb_in:*
4: gb_om:*
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9: gb_pr:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	80.0	427	1	AF621974 Unculture
2	16	80.0	427	1	AF621974 Unculture
3	16	80.0	429	1	AF621971 Unculture
4	16	80.0	429	1	AF621971 Unculture
5	16	80.0	745	1	AY102896 Unculture
6	16	80.0	745	1	AY102896 Unculture
7	16	80.0	814	1	U8A367881
8	16	80.0	814	1	U8A367881
9	16	80.0	197358	2	AC136479 Mus muscu
10	16	80.0	197358	2	AC136479 Mus muscu
11	16	80.0	210346	2	EX511154 Danio rer
12	16	80.0	210346	2	EX511154 Danio rer
13	16	80.0	244788	5	EX511023 Zebrafish
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15	16	75.0	504	1	AF261058 Gelidibac
16	16	75.0	504	1	AF261058 Gelidibac
17	16	75.0	1394	1	AY162084 Bacteroid
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19	16	75.0	1426	1	AF218782 Muricauda

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C 21	15	75.0	1491	1	AF300973 Bacterium
C 22	15	75.0	1491	1	AF300973 Bacterium
C 23	15	75.0	190588	2	AC141720 Agis mell
C 24	15	75.0	190588	2	AC141720 Agis mell
C 25	15	75.0	191208	2	AC138026 Mus muscu
C 26	15	75.0	191208	2	AC138026 Mus muscu
C 27	15	75.0	221150	2	AC134589 Mus muscu
C 28	15	75.0	221150	2	AC134589 Mus muscu
C 29	15	75.0	300399	1	AE016764 Escherich
C 30	15	75.0	300399	1	AE016764 Escherich
C 31	15	75.0	349723	1	EX842650 Bdeliobib
C 32	15	75.0	349723	1	EX842650 Bdeliobib
C 33	14	70.0	376	1	AY006723 Unculture
C 34	14	70.0	376	1	AY006723 Unculture
C 35	14	70.0	499	1	AB028348 Unidentif
C 36	14	70.0	499	1	AB028348 Unidentif
C 37	14	70.0	499	1	AB028358 Unidentif
C 38	14	70.0	499	1	AB028358 Unidentif
C 39	14	70.0	503	1	AB121810 Streptoco
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C 41	14	70.0	517	1	AB028427 Unidentif
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C 44	14	70.0	529	1	AB064836 Unculture
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ALIGNMENTS

RESULT 1	AF621974	427 bp	DNA	linear	ECT 23-JUL-2004
LOCUS	AF621974				
DEFINITION	Uncultured bacterium partial 16S rRNA gene, clone IRR-D57-20.				
ACCESSION	AF621974				
VERSION	AF621974.1	GI:50582380			
KEYWORDS	16S ribosomal RNA; 16S rRNA gene.				
SOURCE	uncultured bacterium				
ORGANISM	Bacteria; environmental samples.				
REFERENCE	1				
AUTHORS	Scheid D., Stubner S. and Conrad R.				
TITLE	Identification of rice root associated nitrate, sulfate and ferric iron reducing bacteria				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 427)				
AUTHORS	Scheid D.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-JAN-2004) Scheid D., Biogeochemistry, MPI for Terrestrial Microbiology, Karl-Von-Frisch Str., D-35043 Marburg, GERMANY				
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source	1..427				
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Query Match	80.0%; Score 16; DB 1; length 427;				
Best Local Similarity	100.0%; Pred. No. 52;				
Matches	16; Conservative 0; Mismatches 0; Gaps 0;				
QY	5 TGGCATTCGATGAT 20				

Db 144 TGCATATCGCATGAT 159

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AJ621974/c 427 bp DNA linear BCT 23-JUL-2004
LOCUS Uncultured bacterium partial 16S rRNA gene, clone IRR-DS7-20.
DEFINITION
AJ621974
ACCESSION
AJ621974.1 GI:50582380
VERSION
16S ribosomal RNA; 16S rRNA gene.
KEYWORDS
uncultured bacterium
SOURCE
uncultured bacterium
ORGANISM
Bacteria; environmental samples.
REFERENCE
1 Scheid,D., Stubner,S. and Conrad,R.
AUTHORS Identification of rice root associated nitrate, sulfate and ferric
TITLE iron reducing bacteria
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 427)
TITLE Scheid,D.
REFERENCE Direct Submission
AUTHORS Submitted (23-JAN-2004) Scheid D., Biogeochemistry, MPI for
JOURNAL Terrestrial Microbiology, Karl-Von-Frisch Str., D-35043 Marburg,
GERMANY

FEATURES
source Location/Qualifiers
1..427

gene
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ORIGIN

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Best Local Similarity 100.0%; Pred.No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCATGCGATATCGCA 16
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Db 159 ATCATGCGATATCGCA 144

RESULT 3
AJ621971 429 bp DNA linear BCT 23-JUL-2004
LOCUS Uncultured bacterium partial 16S rRNA gene, clone IRR-DS7-8.
DEFINITION
AJ621971
ACCESSION
AJ621971.1 GI:50582377
VERSION
16S ribosomal RNA; 16S rRNA gene.
KEYWORDS
uncultured bacterium
SOURCE
uncultured bacterium
ORGANISM
Bacteria; environmental samples.
REFERENCE
1 Scheid,D., Stubner,S. and Conrad,R.
AUTHORS Identification of rice root associated nitrate, sulfate and ferric
TITLE iron reducing bacteria
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 429)
TITLE Scheid,D.
REFERENCE Direct Submission
AUTHORS Submitted (23-JAN-2004) Scheid D., Biogeochemistry, MPI for
JOURNAL Terrestrial Microbiology, Karl-Von-Frisch Str., D-35043 Marburg,
GERMANY

FEATURES
source Location/Qualifiers
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Query Match 80.0%; Score 16; DB 1; Length 429;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGCATATCGCATGAT 20
|||||
Db 144 TGCATATCGCATGAT 159

RESULT 4
AJ621971/c 429 bp DNA linear BCT 23-JUL-2004
LOCUS Uncultured bacterium partial 16S rRNA gene, clone IRR-DS7-8.
DEFINITION
AJ621971
ACCESSION
AJ621971.1 GI:50582377
VERSION
16S ribosomal RNA; 16S rRNA gene.
KEYWORDS
uncultured bacterium
SOURCE
uncultured bacterium
ORGANISM
Bacteria; environmental samples.
REFERENCE
1 Scheid,D., Stubner,S. and Conrad,R.
AUTHORS Identification of rice root associated nitrate, sulfate and ferric
TITLE iron reducing bacteria
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 429)
TITLE Scheid,D.
REFERENCE Direct Submission
AUTHORS Submitted (23-JAN-2004) Scheid D., Biogeochemistry, MPI for
JOURNAL Terrestrial Microbiology, Karl-Von-Frisch Str., D-35043 Marburg,
GERMANY

FEATURES
source Location/Qualifiers
1..429

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Best Local Similarity 100.0%; Pred.No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCATGCGATATCGCA 16
|||||
Db 159 ATCATGCGATATCGCA 144

RESULT 5
AY102896 745 bp DNA linear BCT 24-JUN-2002
LOCUS Uncultured bacterium clone BCM3P-27B 16S ribosomal RNA gene,
DEFINITION

Result No.	Score	Query Length	DB	ID	Description
1	16	80.0	569	7	CC010324
2	16	80.0	731	7	CC015681
3	16	80.0	770	7	CF812011
4	16	80.0	773	7	CC017170
5	16	80.0	798	7	CC034183
6	16	80.0	811	7	CC0319122
7	16	80.0	864	7	CC022163
8	16	80.0	864	7	CC033025
9	16	80.0	927	7	CC020014
10	16	80.0	941	7	CC021731
11	16	80.0	944	7	CC032174
12	16	80.0	974	7	CC022893
13	16	80.0	1008	7	CC026836
14	16	80.0	1009	7	CC033329
15	15	75.0	156	7	CK099767
16	15	75.0	162	9	CG198199
17	15	75.0	264	1	AV292574
18	15	75.0	271	5	BK765596
19	15	75.0	278	4	BMS582521
20	15	75.0	283	5	BK604726
21	15	75.0	304	5	BK766921
22	15	75.0	305	5	BK603239
23	15	75.0	328	5	BK765460
24	15	75.0	383	9	CC467657

25	15	75.0	457	5	EX614015	BX614015	EX614015
26	15	75.0	517	5	EX606907	BX606907	EX606907
27	15	75.0	519	4	BM611632	BM611632	170006871
28	15	75.0	529	8	BH450732	BH450732	BOHCT76BR
29	15	75.0	531	5	EX716735	BX766735	EX766735
30	15	75.0	540	5	BZ145896	SP_0015	B
31	15	75.0	545	8	EX616446	BX616446	EX616446
32	15	75.0	546	5	AZ3064016	BX614016	EX614016
33	15	75.0	552	8	AZ306453	AZ306453	1M0007J01
34	15	75.0	555	4	BM590645	BM590645	170006873
35	15	75.0	556	5	EX604558	BX604558	EX604558
36	15	75.0	563	8	BZ415598	BZ415598	1457B05.9
37	15	75.0	568	8	AQ717776	HS_5507	B
38	15	75.0	588	5	EUT71886	BUT71886	SJM2BSD01
39	15	75.0	591	4	BM599323	170006873	BM599323
40	15	75.0	592	9	CG413516	CG413516	ZMMBB027
41	15	75.0	602	9	CG799749	CG799749	1718004D1
42	15	75.0	609	4	BM581510	BM581510	170006872
43	15	75.0	610	6	CD744877	IRB7_001	CD744877
44	15	75.0	614	5	EX604307	EX604307	EX604307
45	15	75.0	622	4	BM657349	BM657349	170006874

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE
CC010324	CC010324	569 bp mRNA linear EST 09-JUN-2004	CC010324	CC010324	GI:48517213	Coccidioides posadasii	Coccidioides posadasii	1 (bases 1 to 569)
		EST798659 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3 kb Coccidioides posadasii cDNA clone C18391 3' end, mRNA sequence.					Enkaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.	Gardner M. I. and Cole G. T.

REVIEWED	2003-11-13	13
TITLE	Analysis of gene expression in <i>Coccidioides posadasii</i> mycelia and spherules via expressed sequence tags	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Gardner MJ	

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel.: 301 838 3519
Fax: 301 838 0208
Email: garciare@tigr.org.

FEATURES	Location/Qualifiers
1	ECO

```

source
1. :369
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0.4 to 2.3 kb"
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kb"

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ORIGIN

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Query Match:      80.0%;  Score 16;  DB 7;  Length 569;
Best Local Similarity 100.0%;  Pred. No. 8.7;
Matches 16;  Conservative 0;  Indels 0;  Gaps 0

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QY      1 ATCATGGGATATCATG 16
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Db      38 ATCATGGGATATCATG 53

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RESULT 2          731 bp      mRNA      linear      EST 09-JUN-2004
LOCUS             CCO015681
DEFINITION        Coccidioides posadasii saprobic phase cDNA library,
                  greater than 4kb Coccidioides posadasii cDNA clone CIBA171 3', end,
                  mRNA sequence.
ACCESSION         CCO015681
VERSION           CCO015681.1
KEYWORDS          GI:46522570
SOURCE            EST.
ORGANISM          Coccidioides posadasii
                  Coccidioides posadasii
                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                  Omygenales; mitosporic Omygenales; Coccidioides.
REFERENCE         1 (bases 1 to 731)
AUTHORS           Gardner M.J. and Cole G.T.
TITLE             Analysis of gene expression in Coccidioides posadasii mycelia and
                  spherules via expressed sequence tags
JOURNAL           Unpublished (2003)
COMMENT           Other ESTs: EST786064
                  Contact: Gardner MJ
                  The Institute for Genomic Research
                  9712 Medical Center Drive, Rockville, MD 20850, USA
                  Tel: 301 838 3519
                  Fax: 301 838 0208
                  Email: gardner@tigr.org
FEATURES
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ORIGIN
Query Match      80.0%; Score 16; DB 7; Length 731;
Best Local Similarity 100.0%; Pred. No. 8 7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY               1 ATCATGCGATATCATG 16
DB               310 ATCATGCGATATCATG 325
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LOCUS             CFB12011
DEFINITION        CFB12011
                  770 bp      mRNA      linear      EST 01-APR-2004
                  EST689393 Coccidioides posadasii saprobic phase cDNA library,
                  greater than 4kb Coccidioides posadasii cDNA clone CIBA171 3', end,
                  mRNA sequence.
ACCESSION         CFB12011
VERSION           CFB12011.1
KEYWORDS          GI:45917889
SOURCE            EST.
ORGANISM          Coccidioides posadasii
                  Coccidioides posadasii
                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                  Omygenales; mitosporic Omygenales; Coccidioides.
REFERENCE         1 (bases 1 to 770)
AUTHORS           Gardner M.J. and Cole G.T.
TITLE             Analysis of gene expression in Coccidioides posadasii mycelia and
                  spherules via expressed sequence tags
JOURNAL           Unpublished (2003)
COMMENT           Other ESTs: EST689394
                  Contact: Gardner MJ
                  The Institute for Genomic Research
                  9712 Medical Center Drive, Rockville, MD 20850, USA

```

```

Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@igf.org
location/Qualifiers
FEATURES
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/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIBB586"
/dev_stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, Ti phase resistant"
/clone_lib="Coccidioides posadasii saprobic phase cDNA library, greater than 4kb"
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ORIGIN
Query Match 80.0%; Score 16; DB 7; Length 773;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
LOCUS C0017170 773 bp mRNA linear EST 09-JUN-2004
DEFINITION EST787552 Coccidioides posadasii saprobic phase cDNA library, greater than 4kb Coccidioides posadasii cDNA clone CIBB586 5' end, mRNA sequence.
C0017170
C0017170.1 GI:48524059
EST.
Coccidioides posadasii
Coccidioides posadasii
Buxarjota, Furg.; Ascomycota, Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
1 (bases 1 to 773)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags
Unpublished (2003)
Other ESTs: EST787551
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@igf.org
Seq primer: M13 Reverse.
location/Qualifiers
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/lab_host="E. coli DH10B, Ti phase resistant"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 11:48:05 ; Search time 166.5 Seconds
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623.077 Million cell updates/sec

Title: SEQ4-4

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 413486 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	467	6 ABL39818	ABL39818 Human NS
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3	14	70.0	162	12 ACH93501	ACH93501 Human gen
4	14	70.0	417	8 ABX43931	ABX43931 Bovine ES
5	14	70.0	510	12 ACH79801	ACH79801 Human gen
6	14	70.0	1000	4 AAF91415	AAF91415 DNA seque
7	14	70.0	1000	6 ABK37795	ABK37795 DNA seque
8	14	70.0	1029	10 ADB79861	ADB79861 Mouse SGC
9	14	70.0	1044	12 ADL02524	ADL02524 DNA encod
10	14	70.0	1086	12 ADL02896	ADL02896 DNA encod
11	14	70.0	1578	4 AAH57572	AAH57572 Human bra
12	14	70.0	1654	10 ABT42291	ABT42291 Toxicity
13	14	70.0	1810	10 ADB62769	ADB62769 Human cDN
14	14	70.0	1865	6 ABU39816	ABU39816 Human NS
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20	14	70.0	9099	6 AAS16809	AAS16809 Penicilli
21	14	70.0	14483	8 ACC48945	ACC48945 Escherich

22	14	70.0	34203	4 AAF74546	AAF74546 Penicilli
23	14	70.0	34203	6 AAS16770	AAS16770 Penicilli
24	14	70.0	34263	4 AAF74547	AAF74547 Penicilli
25	14	70.0	72149	10 ADE81173	ADE81173 ML-236B s
26	14	70.0	89047	4 AAF28547	AAF28547 genomic f
27	14	70.0	99629	4 AAF28550	AAF28550 genomic f
28	14	70.0	110000	10 ACF67367	ACF67367 Continuation (17 o
29	14	70.0	110000	10 ACF65388_11	ACF65388_11 Continuation (12 o
30	13	65.0	27	20 AAV21928	AAV21928 Nuclease
31	13	65.0	239	12 ADL60151	ADL60151 Rat cDNA
32	13	65.0	270	12 ADL60195	ADL60195 Cat cDNA
33	13	65.0	492	6 ABN92710	ABN92710 Scaphyloc
34	13	65.0	504	3 AA251989	AA251989 Salmonell
35	13	65.0	574	12 ACH80026	ACH80026 Human gen
36	13	65.0	686	2 AAG78205	AAG78205 Gene codi
37	13	65.0	737	2 ADR02240	ADR02240 A. gossyp
38	13	65.0	795	10 ABX07363	ABX07363 S. pneumo
39	13	65.0	891	6 AAD35513	AAD35513 Pantoea s
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ALIGNMENTS

RESULT 1	ABL39818	standard; cDNA; 467 bp.
ID	ABL39818	
AC	ABL39818;	
XX		
DT	10-MAY-2002	(first entry)
XX		
DE	Human NS cDNA sequence SEQ ID NO:128.	
XX		
XX	Human; cytostatic; osteopathic; gynaecological; neuroprotective;	
KW	antithrombotic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;	
KW	vasoregulator; antiarteriosclerotic; antiinflammatory; dermatological;	
KW	anorectic; muscular; antiferility; cardiovascular; anticonvulsant;	
KW	antifibrinolytic; hypotension; antiasratic; immunomodulator; cardiac;	
KW	anticonvulsant; antidiabetic; tranquilizer; antidepressant; neuroleptic;	
KW	gastrointestinal; virucide; antitumor; cerebroprotective; nootropic;	
KW	contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;	
KW	endometriosis; degenerative disease; multiple sclerosis; psoriasis;	
KW	rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;	
KW	inflammation; skin disorder; obesity; muscular dystrophy; AIDS;	
KW	infertility; cardiovascular disease; coagulation disease; hypertension;	
KW	ischemia; asthma; immune disease; epilepsy; angina; neurodegeneration;	
KW	diabetes; anxiety; depression; schizophrenia; viral disease; stroke;	
KW	gastric ulcer; Alzheimer's disease; gene; ss.	
OS	Homo sapiens.	
XX		
PN	W0200206315-A2.	
XX		
PD	24-JAN-2002.	
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PF	17-JUL-2001; 2001WC-11000653.	
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PR	18-JUL-2000; 2000IL-00137345.	
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PR	15-DEC-2000; 2000IL-00140354.	
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PA	(COMP-) COMPUGEN LTD.	
XX		
PI	Mintz L, Freilich S, Bernstein J;	
XX		
DR	WPI; 2002-155037/20.	
XX		
DR	P-PSDB; ABB06164.	
XX		

PT One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
 PS Claim 1; Page 148; 290pp; English.

XX ABL39693 to ABL39818 represent novel human nucleic acid sequences
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 CC (NS) can have cytosstatic, osteopathic, gynaecological, neuroprotective,
 CC antirheumatic, antidiabetic, antipsoriatic, ophthalmological, virocidic,
 CC vasorelaxant, antiarteriosclerotic, antiinflammatory, dermatological,
 CC anorectic, muscular, anti-HIV, antinfertility, cardiovascular, cardiant,
 CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, antiulcer,
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilizer, antiulcer,
 CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
 CC neurotropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive

SQ Sequence 467 BP; 144 A; 101 C; 112 G; 110 T; 0 U; 0 Other;
 QY Query Match 100.0%; Score 20; DB 6; Length 467;
 Best Local Similarity 100.0%; Pred. No. 0.008;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 ATCATGCGATATCATGCGAT 20
 401 ATCATGCGATATCATGCGAT 420

RESULT 2
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XX ABL39817;
 XX
 DT 10-MAY-2002 (first entry)

DE Human NS cDNA sequence SEQ ID NO:127.

XX Human; cytosstatic; osteopathic; gynaecological; neuroprotective;
 KM antirheumatic; antidiabetic; antipsoriatic; ophthalmological; anti-HIV;
 KM vasorelaxant; antiarteriosclerotic; antiinflammatory; dermatological;
 KM anorectic; muscular; anti-HIV; antinfertility; cardiovascular; cardiant;
 KM antifibrinolytic; hypotension; antiasthmatic; immunomodulator; antiulcer;
 KM anticonvulsant; antidiabetic; tranquilizer; antidepressant; neuroleptic;
 KM gastrointestinal; virocidic; antiulcer; cerebroprotective; neurotropic;
 KM contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
 KM endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KM rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
 KM inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KM infertility; cardiovascular disease; coagulation disease; hypertension;
 KM ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
 KM diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KM gastric ulcer; Alzheimer's disease; gene; ss.

OS Homo sapiens.
 XX
 PN WO200206315-A2.
 XX
 PD 24-JAN-2002.

XX 17-JUL-2001; 2001WO-11000653.

XX 18-JUL-2000; 2000IL-00137345.
 PR 15-DEC-2000; 2000IL-00140354.
 PR

XX (COMP-) COMPUSEN LTD.
 PA Mintz L, Freilich S, Bernstein J;
 XX
 PI
 XX
 DR WPI: 2002-155037/20.
 DR P-PsDB: ABB06163.

PT One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
 PS Claim 1; Page 148; 290pp; English.

XX ABL39691 to ABL39818 represent novel human nucleic acid sequences
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 CC (NS) can have cytosstatic, osteopathic, gynaecological, neuroprotective,
 CC antirheumatic, antidiabetic, antipsoriatic, ophthalmological, virocidic,
 CC vasorelaxant, antiarteriosclerotic, antiinflammatory, dermatological,
 CC anorectic, muscular, anti-HIV, antinfertility, cardiovascular, cardiant,
 CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, antiulcer,
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilizer, antiulcer,
 CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
 CC neurotropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive

SQ Sequence 468 BP; 144 A; 101 C; 113 G; 110 T; 0 U; 0 Other;
 QY Query Match 100.0%; Score 20; DB 6; Length 468;
 Best Local Similarity 100.0%; Pred. No. 0.008;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATGCGATATCATGCGAT 20
 Db 402 ATCATGCGATATCATGCGAT 421

RESULT 3
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XX ACH93501;
 XX
 DT 29-JUL-2004 (first entry)

DE Human genome derived single exon probe #26696.

XX Human; probe; ss; gene expression; single exon probe; microarray;
 KM alternative splicing event; genomic alteration.

OS Homo sapiens.
 XX
 PN US2003194704-A1.
 XX
 PD 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 PI Penn SG, Rank DR, Hanzel DK;

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PR	08-NOV-2000	2000US-0246454P
PR	08-NOV-2000	2000US-0246455P
PR	08-NOV-2000	2000US-0246476P

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;
WPI; 2001-541565/50.

Nucleic acids encoding 3224 human nervous system antigen polypeptides,
useful for preventing, diagnosing and/or treating nervous system cancers
and metastases.

Disclosure; SEQ ID NO i2437; 1701bp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins
(ABAI1678-ABBI6001) useful for preventing, treating or ameliorating
medical conditions e.g. by protein or gene therapy. The genes are
isolated from a range of human tissues disclosed in the specification.
The nucleic acids, proteins, antibodies and (antagonists are useful in
the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
breast), gastrointestinal tract, liver, lung, or urogenital; (b) immune
disorders e.g. Addison's disease, allergies, autoimmune haemolytic
anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
cardiovascular disorders such as myocardial ischemias; (d) wound healing
infectious diseases such as viral, bacterial, fungal and parasitic
infections. Note: The sequence data for this patent did not form part of

Thu Oct 28 08:00:18 2004

seq1-cl.rge

Page 1

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OM nucleic - nucleic search, using sw model

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(without alignments)
1331.870 Million cell updates/sec

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Perfect score: 20
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Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 0 9053458

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	19	95.0	251124	9	HUAE000660	AE000660 Homo sapi
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4	18	90.0	171263	10	AC118702	AC118702 Mus muscu
5	18	90.0	234203	2	AC121311	AC121311 Mus muscu
6	18	90.0	234203	2	AC121311	AC121311 Mus muscu
7	17	85.0	6172	1	MTWCR	X07794 M. chertocau
8	17	85.0	6172	1	MTWCR	X07794 M. chertocau
9	17	85.0	97011	9	HS997015	AL035073 Human DNA
10	17	85.0	97011	9	HS997015	AL035073 Human DNA
11	17	85.0	134995	2	AC122494	AC122494 Mus muscu
12	17	85.0	134995	2	AC122494	AC122494 Mus muscu
13	17	85.0	136839	9	AL139397	AL139397 Human DNA
14	17	85.0	136839	9	AL139397	AL139397 Human DNA
15	17	85.0	161266	10	AC127298	AC127298 Mus muscu
16	17	85.0	161266	10	AC127298	AC127298 Mus muscu
17	17	85.0	173849	9	AC078855	AC078855 Homo sapi
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19	17	85.0	175464	9	AC069021	AC069021 Homo sapi

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c	24	17	85.0	198756	9	AC087575	AC087575 Homo sapi
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c	26	17	85.0	195035	2	AC022263	AC022263 Homo sapi
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c	30	17	85.0	216523	9	AC073587	AC073587 Homo sapi
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c	32	17	85.0	243707	2	AC126141	AC126141 Rattus no
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ALIGNMENTS

RESULT 1	HUAE000660	251124 bp	DNA	linear	PRI 19-DEC-2002
LOCUS	Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.				
DEFINITION	AE000660 AE000521 U85197				
ACCESSION	AE000660.1 GI:2358042				
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 251124)				
AUTHORS	Koop, B.F., Rowen, L., Wang, K., Kuo, C.L., Seto, D., Lenstra, J.A., Howard, S., Shan, W., Deshpande, P., and Hood, L.				
TITLE	The human T-cell receptor TCRAC/TCRDC (C alpha/C delta) region: Organization, sequence, and evolution of 97.6 kb of DNA				
JOURNAL	Genomics 19 (3), 478-493 (1994)				
MEDLINE	94245236				
PUBMED	8188290				
REFERENCE	2 (bases 1 to 251124)				
AUTHORS	Boysen, C., Simon, M.I., and Hood, L.				
TITLE	Analysis of the 1.1-Mb human alpha/delta T-cell receptor locus with bacterial artificial chromosome clones				
JOURNAL	Genome Res. 7 (4), 330-338 (1997)				
MEDLINE	97264339				
PUBMED	9110172				
REFERENCE	3 (bases 1 to 251124)				
AUTHORS	Boysen, C., Inyoni, L., Smith, T.M., Smit, A., Wang, K., Rowen, L., and Hood, L.				
TITLE	T-Cell Receptor Alpha Delta Locus Complete Nucleotide Sequence Unpublished				
JOURNAL	This citation covers bases 1-983545 and bases 1064020-1071650				
REFERENCE	4 (bases 1 to 251124)				
AUTHORS	Boysen, C., Lee, I., Smith, T.M., Smit, A., Kai, W., Lee, R., and Leroy, H.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUN-1997) Department of Molecular Biotechnology, University of Washington, Box 357730, Seattle, Washington 98195, USA				
REMARK	Complete nucleotide sequence of the human T-cell receptor alpha delta locus				

Thu Oct 28 08:00:18 2004

seq1-cl.rge

Page 2

COMMENT On Jun 12, 2001 this sequence version replaced gi:2121231.
Sequencing method: high redundancy shotgun. Interspersed Repeats
were identified with RepeatMasker (available from
http://ftp.genome.washington.edu/RM/RepeatMasker.html) Simple
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http://serac.mbt.washington.edu/~chrisa/software/sputnik.html).
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Mintz, L., Freilich, S. and Bernstein, J.
TITLE Novel nucleic acid and amino acid sequences
JOURNAL Patent: WO 0206315-A 127 24-JAN-2002;
COMPUGEN Ltd. (IL)
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DEFINITION [human, embryo, mRNA, 696 nt].
ACCESSION 582024
VERSION 582024.1 GI:1478502
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS Okazaki, T., Wang, H., Masliyah, E., Cao, M., Johnson, S. A., Sundsmo, M.,
Saitoh, T. and Mori, N.
TITLE SCG10, a neuron-specific growth-associated protein in Alzheimer's
disease
JOURNAL Neurobiol. Aging 16 (6), 883-894 (1995)
MEDLINE 96192978
PUBMED 8622778
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gisbseq 177683] from the original journal article.
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Mintz, L., Freilich, S. and Bernstein, J.
TITLE Novel nucleic acid and amino acid sequences
JOURNAL Patent: WO 0206315-A 127 24-JAN-2002;
COMPUGEN Ltd. (IL)
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DB 421 ATCGCATGATATCGCATGAT 402
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582024 696 bp mRNA linear PRI 03-ANG-1996
LOCUS SCG10=neuron-specific growth-associated protein/strathmin homolog
DEFINITION [human, embryo, mRNA, 696 nt].
ACCESSION 582024
VERSION 582024.1 GI:1478502
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS Okazaki, T., Wang, H., Masliyah, E., Cao, M., Johnson, S. A., Sundsmo, M.,
Saitoh, T. and Mori, N.
TITLE SCG10, a neuron-specific growth-associated protein in Alzheimer's
disease
JOURNAL Neurobiol. Aging 16 (6), 883-894 (1995)
MEDLINE 96192978
PUBMED 8622778
REMARK Genbank staff at the National Library of Medicine created this
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seq2-c2.rst

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 12:49:40 : Search time 1408.75 Seconds
(without alignments)
517.334 Million cell updates/sec

Title: SEQ2-C2
Perfect score: 20
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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VERSION	CG137880.1	GI:34026663			
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ORGANISM	Zea mays				
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REFERENCE	White, C.A., Quackenbush, J., Van Aken, S., Utreback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.				
AUTHORS	Maize Genomics Consortium				
TITLE	Unpublished (2003)				
JOURNAL	Other GSS: PUJEX65TD				
COMMENT	Contact: Cathy White, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitec@tigr.org Seq primer: IR Class: sheared ends.				
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seq2-c2.rst

Page 2

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VERSION
CG137880.1 GI:34028663
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SOURCE
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ORGANISM
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 797)
White, C.A., Quackenbush, J., Van Aken, S., Uteback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
REFERENCE
AUTHORS
White, C.A., Quackenbush, J., Van Aken, S., Uteback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUBX657B
CONTACT: Cathy White, cwhite@tigr.org
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white@tigr.org
Seq primer: TR
Class: sheared ends.
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VERSION
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clade; Panicoideae; Andropogoneae; Zea.
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White, C.A., Quackenbush, J., Van Aken, S., Uteback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
REFERENCE
AUTHORS
White, C.A., Quackenbush, J., Van Aken, S., Uteback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUBN437B
CONTACT: Cathy White, cwhite@tigr.org
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white@tigr.org
Seq primer: TR
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white@tigr.org
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COT selected genomic DNA library"
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|||||
RESULT 4
CG069001/c 946 bp DNA linear GSS 19-AUG-2003
PUBN437D_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZMWBTA0687H14,
DEFINITION
genomic survey sequence.
ACCESSION
CG069001
VERSION
CG069001.1 GI:33941181
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 946)
White, C.A., Quackenbush, J., Van Aken, S., Uteback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
REFERENCE
AUTHORS
White, C.A., Quackenbush, J., Van Aken, S., Uteback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUBN437B
CONTACT: Cathy White, cwhite@tigr.org
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
1..946
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZM_0.6_1.0_KB"
/clone_1ib="ZM_0.6_1.0_KB"
/Note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
ORIGIN
Query Match 90.0%; Score 18; DB 9; Length 946;
Best Local Similarity 100.0%; Pred.No.0.051;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCAGTCGATATCGACTG 18
|||||
```

Thu Oct 28 08:00:21 2004

seq2-c2.rge

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: October 27, 2004, 11:49:55 ; Search time 710.125 Seconds
(without alignments)
1331.870 Million cell updates/sec

Title: SEQ2-C2

Perfect score: 20

Sequence: 1 atcagtcgacatcgcactgat 20

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	80.0	64915	5 AC091300	Danio rer
2	16	80.0	64915	5 AC091300	Danio rer
3	16	80.0	178225	5 BX005286	zebrafish
4	16	80.0	178225	5 BX005286	zebrafish
5	16	80.0	207611	2 BX004968	Danio rer
6	16	80.0	207611	2 BX004968	Danio rer
7	16	80.0	303250	1 AP001518	Bacillus
8	16	80.0	303250	1 AP001518	Bacillus
9	16	75.0	9179	1 AE014584	Bacillus
10	16	75.0	9179	1 AE014584	Bacillus
11	15	75.0	10362	1 AE011178	Methanosa
12	15	75.0	10362	1 AE011178	Methanosa
13	15	75.0	12244	1 AE009676	Bruceella
14	15	75.0	12244	1 AE009676	Bruceella
15	15	75.0	51601	7 AY374448	Bacterioph
16	15	75.0	51601	7 AY374448	Bacterioph
17	15	75.0	55856	5 BX276102	zebrafish
18	15	75.0	55856	5 BX276102	zebrafish
19	15	75.0	59820	2 BX649285_3	Continuation (4 of

20	15	75.0	59820	2 BX649285_3	Continuation (4 of
21	15	75.0	91609	5 BX323023	zebrafish
22	15	75.0	91609	5 BX323023	zebrafish
23	15	75.0	102704	5 AL672216	zebrafish
24	15	75.0	102704	5 AL672216	zebrafish
25	15	75.0	110590	5 BX001021	zebrafish
26	15	75.0	110590	5 BX001021	zebrafish
27	15	75.0	114157	5 BX294157	zebrafish
28	15	75.0	114157	5 BX294157	zebrafish
29	15	75.0	114924	2 AC148786	zebrafish
30	15	75.0	114924	2 AC148786	zebrafish
31	15	75.0	126202	5 AL591427	zebrafish
32	15	75.0	126202	5 AL591427	zebrafish
33	15	75.0	128296	5 BX897690	zebrafish
34	15	75.0	128296	5 BX897690	zebrafish
35	15	75.0	140382	5 BX842684	zebrafish
36	15	75.0	140382	5 BX842684	zebrafish
37	15	75.0	145496	2 CR545470	Danio rer
38	15	75.0	145496	2 CR545470	Danio rer
39	15	75.0	145777	2 BX511166	Danio rer
40	15	75.0	145777	2 BX511166	Danio rer
41	15	75.0	146052	2 CR384049	Danio rer
42	15	75.0	146052	2 CR384049	Danio rer
43	15	75.0	146575	2 BX957262	Danio rer
44	15	75.0	146575	2 BX957262	Danio rer
45	15	75.0	150351	2 BX247899	Danio rer

ALIGNMENTS

RESULT 1	AC091300	64915 bp	DNA	linear	VRT 16-OCT-2002
LOCUS	AC091300				
DEFINITION	Danio rerio clone 127K3, complete sequence.				
ACCESSION	AC091300.3	GI:24022405			
VERSION	AC091300.3	GI:24022405			
KEYWORDS	HTG.				
SOURCE	Danio rerio (zebrafish)				
ORGANISM	Danio rerio				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
AUTHORS	1 (bases 1 to 64915) Aylele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,U., Ho,S.-L., Idol,J.R., Karlins,E., Lee-Lin,S.-O., Legaspi,R., Lim,M., Maduro,Q.L., Maduro,V.B., Masello,C., Mastrian,S.D., McCloskey,J.C., McDowell,U., Pearson,R., Prasad,A., Shevchenko,Y., Snyder,B., Stantipop,S., Thomas,U.W., Thomas,P.J., Touchman,J.W., Tsurguen,C., Vogt,U.L., Walker,M.A., Welherby,K.D., Zhang,H.-H. and Green,E.D.				
REFERENCE	NISC Comparative Sequencing Initiative				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 64915)				
REFERENCE	Green,E.D.				
AUTHORS	Submitted (13-APR-2001) NIH Intramural Sequencing Center, 8717				
TITLE	Direct Submission				
JOURNAL	Submitted (07-JUL-2001) NIH Intramural Sequencing Center, 8717				
REFERENCE	Groveomont Circle, Galtersburg, MD 20877, USA				
AUTHORS	4 (bases 1 to 64915)				
TITLE	Direct Submission				
JOURNAL	Submitted (16-OCT-2002) NIH Intramural Sequencing Center, 8717				
REFERENCE	Groveomont Circle, Galtersburg, MD 20877, USA				
AUTHORS	On Oct 16, 2002 this sequence version replaced gi:14626272.				
COMMENT	Center: NIH Intramural Sequencing Center				
	Center code: NISC				

Web site: <http://www.nisc.nih.gov>
 Contact: nisc.zoo@nih.gov
 ----- Project Information
 Center project name: aql
 Center clone name: 127K03

This sequence was finished as follows unless otherwise noted:
 all regions were double-stranded, sequenced with an
 alternate chemistry, or covered by high quality data
 (i.e., phred quality >= 30); an attempt was made to resolve
 all sequencing problems, such as compressions and repeats;
 all regions were covered by at least one plasmid subclone
 or more than one M13 subclone; and the assembly was confirmed
 by restriction digest.

CLONE LENGTH: This sequence represents the entire insert of
 this clone unless otherwise noted. If there are overlapping
 clones, the overlaps are noted in the beginning and end of
 the Features section.

FEATURES
 source
 1..64915
 /organism="Danio rerio"
 /mol_type="Genomic DNA"
 /db_xref="taxon:7955"
 /clone_1b="127K3"
 /clone_1lb="Incyte Genomics"
 26404..26418
 /note="single clone coverage"

ORIGIN
 Query Match 80.0%; Score 16; DB 5; Length 64915;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGATATGACCTGAT 20
 |||||
 54116 GTGATATGACCTGAT 54131

RESULT 2
 AC091300/c 64915 bp DNA linear VRT 16-OCT-2002
 LOCUS Danio rerio clone 127K3, complete sequence.
 AC091300
 AC091300.3 GI:24022405
 VERSION HTG.
 KEYWORDS
 SOURCE Danio rerio (zebrafish)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 64915)
 Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
 Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.B.,
 Grante, S., Guan, X., Gupta, D., Ho, S.-L., Idoi, J.R., Karlins, E.,
 Lee-Jin, S.-O., Legaspi, R., Lim, M., Maduro, O.L., Maduro, V.B.,
 Masello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J.,
 Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantrisp, S.,
 Thomas, W.W., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, C.L.,
 Walker, M.A., Wetherby, K.D., Zhang, L.-H., and Green, E.D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 64915)
 Green, E.D.
 Direct Submission
 Submitted (13-APR-2003) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 3 (bases 1 to 64915)
 Green, E.D.
 Direct Submission
 Submitted (07-JUL-2003) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 4 (bases 1 to 64915)

AUTHORS
 Green, E.D.
 Direct Submission
 Submitted (16-SEP-2002) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 On Oct 16, 2002 this sequence version replaced gi:14626272.

COMMENT
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc.zoo@nih.gov
 ----- Project Information
 Center project name: aql
 Center clone name: 127K03

This sequence was finished as follows unless otherwise noted:
 all regions were double-stranded, sequenced with an
 alternate chemistry, or covered by high quality data
 (i.e., phred quality >= 30); an attempt was made to resolve
 all sequencing problems, such as compressions and repeats;
 all regions were covered by at least one plasmid subclone
 or more than one M13 subclone; and the assembly was confirmed
 by restriction digest.

CLONE LENGTH: This sequence represents the entire insert of
 this clone unless otherwise noted. If there are overlapping
 clones, the overlaps are noted in the beginning and end of
 the Features section.

FEATURES
 source
 1..64915
 /organism="Danio rerio"
 /mol_type="Genomic DNA"
 /db_xref="taxon:7955"
 /clone_1b="127K3"
 /clone_1lb="Incyte Genomics"
 26404..26418
 /note="single clone coverage"

ORIGIN
 Query Match 80.0%; Score 16; DB 5; Length 64915;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGTCGATATGAC 16
 |||||
 54131 ATCGTCGATATGAC 54116

RESULT 3
 BX005286 178225 bp DNA linear VRT 23-SEP-2003
 LOCUS zebrafish DNA sequence from clone DKEY-23719, complete sequence.
 AC091300
 BX005286.6 GI:33457028
 VERSION HTG.
 KEYWORDS
 SOURCE Danio rerio (zebrafish)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 178225)
 Heath, P.
 Direct Submission
 Submitted (23-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 fish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Aug 5, 2003 this sequence version replaced gi:33412053.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: fish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.

Query Match	85.0%;	Score 17;	DB 3;	Length 407
Best Local Similarity	100.0%;	Pred. No. 4.2;		

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 TCAGTCGATATCAGTCG 18
 Db 5580 TCAGTCGATATCAGTCG 5596

RESULT 2
 LOCUS AL445195 172064 bp DNA linear PRI 15-DEC-2000
 DEFINITION Human DNA sequence from clone RP11-427013 on chromosome 13,
 complete sequence.

ACCESSION AL445195
 VERSION AL445195.4 GI:11878448
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 172064)
 AUTHORS Dunn, M.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone

COMMENT

On Dec 18, 2000 this sequence version replaced gi:11545086.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated repeat sequence elements. Where the sequence is
 ambiguous, there is an annotation using the 'unsure' feature key.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 13, constructed by the Sanger Centre Chromosome 13
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr13
 RP11-427013 is from the library RP11-11.2 constructed by the group
 of Pieter de Jong. For further details see
 http://www.chori.org/bacpac/home.htm
 VECTOR: pBACE3.6
 This sequence is the entire insert of clone RP11-427013.

FEATURES

source

1..172064
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="13"
 /clone="RP11-427013"
 /clone_1bp="RP11-11.2"
 283..443
 /note="MUT1A2 repeat: matches 1..161 of consensus"
 repeat_region
 457..520
 /note="16 copies 4 mer cctc 85% conserved"
 repeat_region
 527..721
 /note="MUT1A2 repeat: matches 173..374 of consensus"
 repeat_region
 1695..2057
 /note="HAL1 repeat: matches 196..567 of consensus"
 repeat_region
 2265..2478
 /note="112 repeat: matches 2534..2750 of consensus"
 repeat_region
 2479..2598
 /note="FLAM_C repeat: matches 1..111 of consensus"
 repeat_region
 2599..2979
 /note="112 repeat: matches 2175..2534 of consensus"
 repeat_region

repeat_region 3012..3315
 /note="112 repeat: matches 1803..2099 of consensus"
 repeat_region 3391..3438
 /note="12 copies 4 mer cata 75% conserved"
 repeat_region 5972..6119
 /note="37 copies 4 mer aaat 58% conserved"
 repeat_region 6509..6643
 /note="MER90 repeat: matches 5..136 of consensus"
 repeat_region 7417..7708
 /note="ALUSg repeat: matches 1..292 of consensus"
 repeat_region 7882..8514
 /note="L1BP47 repeat: matches 5514..6142 of consensus"
 repeat_region 8771..8877
 /note="L1MA2 repeat: matches 6202..6308 of consensus"
 repeat_region 11129..11365
 /note="MER46A repeat: matches 1..236 of consensus"
 repeat_region 15199..15326
 /note="132 copies 4 mer atct 93% conserved"
 repeat_region 15350..15755
 /note="MST1 repeat: matches 1..426 of consensus"
 repeat_region 16332..16491
 /note="MIR repeat: matches 85..250 of consensus"
 repeat_region 17620..17936
 /note="ALUSg repeat: matches 1..308 of consensus"
 repeat_region 18655..18816
 /note="MUT1J repeat: matches 312..472 of consensus"
 repeat_region 18973..19172
 /note="MER30 repeat: matches 1..200 of consensus"
 repeat_region 19680..20822
 /note="L1M2 repeat: matches -676..619 of consensus"
 repeat_region 20822..21420
 /note="L1 repeat: matches 2331..2981 of consensus"
 repeat_region 21421..21714
 /note="ALUB repeat: matches 1..301 of consensus"
 repeat_region 21715..22215
 /note="L1 repeat: matches 2981..3465 of consensus"
 repeat_region 22194..22215
 /note="L1MA4A repeat: matches 4660..4681 of consensus"
 repeat_region 22216..22522
 /note="ALUSP repeat: matches 1..312 of consensus"
 repeat_region 22523..24006
 /note="L1MA4A repeat: matches 4681..6135 of consensus"
 repeat_region 24192..24481
 /note="ALUSg1 repeat: matches 14..301 of consensus"
 repeat_region 24486..24641
 /note="L1MA4A repeat: matches 6125..6295 of consensus"
 repeat_region 24705..24737
 /note="TIGER2a repeat: matches 412..444 of consensus"
 repeat_region 24744..24897
 /note="TIGER2a repeat: matches 1..259 of consensus"
 repeat_region 25057..25092
 /note="9 copies 4 mer tctg 91% conserved"
 repeat_region 25095..25398
 /note="ALUto repeat: matches 1..286 of consensus"
 repeat_region 25708..26094
 /note="MUT1A2 repeat: matches 1..363 of consensus"
 repeat_region 26502..26814
 /note="112 repeat: matches 1964..2419 of consensus"
 repeat_region 26917..27308
 /note="MST1 repeat: matches 1..425 of consensus"
 repeat_region 28353..28467
 /note="FLAM_A repeat: matches 1..115 of consensus"
 repeat_region 29041..29676
 /note="HSMAR2 repeat: matches 652..1298 of consensus"
 repeat_region 29679..29841
 /note="FRAM repeat: matches -1..161 of consensus"
 repeat_region 29845..29896
 /note="13 copies 4 mer aat 76% conserved"
 repeat_region 29898..30015
 /note="FLAM_C repeat: matches 1..118 of consensus"
 repeat_region 30046..30270
 /note="HSMAR2 repeat: matches 422..644 of consensus"
 repeat_region 30271..30622

```

/note="THIC repeat: matches 1. .371 of consensus"
30623. .30794
/note="HSMAR2 repeat: matches 252. .422 of consensus"
repeat_region
30795. .31170
/note="THIC repeat: matches 1. .371 of consensus"
31171. .31411
/note="HSMAR2 repeat: matches 2. .252 of consensus"
repeat_region
34651. .35102
/note="MER4C repeat: matches 1. .465 of consensus"
repeat_region
35216. .35290
/note="MER53 repeat: matches 7. .82 of consensus"
repeat_region
35291. .35958
/note="MER4A repeat: matches 1. .465 of consensus"
repeat_region
35965. .36068
/note="MER53 repeat: matches 1. .113 of consensus"
repeat_region
36798. .37106
/note="AluY repeat: matches 3. .309 of consensus"
repeat_region
37396. .37443
/note="24 copies 2 mer at 79% conserved"
41913. .42368
/note="L2 repeat: matches 2270. .2749 of consensus"
repeat_region
44620. .44667
/note="24 copies 2 mer tc 72% conserved"
45999. .46780
/note="L1R17 repeat: matches 1. .780 of consensus"
repeat_region
46970. .47275
/note="AluX repeat: matches 1. .305 of consensus"
repeat_region
47305. .47695
/note="L1R7 repeat: matches 1. .449 of consensus"
repeat_region
48464. .48515
/note="26 copies 2 mer ca 86% conserved"
48473. .48516
/note="11 copies 4 mer acac 90% conserved"
48570. .48757
/note="L2 repeat: matches 2114. .2303 of consensus"
repeat_region
48774. .49037
/note="MER7A repeat: matches 68. .336 of consensus"
repeat_region
49073. .49204
/note="23 copies 4 mer atra 59% conserved"
49252. .49331
/note="Tiger3(Goien) repeat: matches 1. .2772 of consensus"
49457. .49778
/note="L1PB2 repeat: matches 5815. .6152 of consensus"
repeat_region
50893. .50966
/note="37 copies 2 mer aa 64% conserved"
53081. .54131
/note="L2 repeat: matches 33. .1147 of consensus"
54270. .54582
/note="AluX repeat: matches 1. .309 of consensus"
54919. .55259
/note="THIC repeat: matches 1. .371 of consensus"
59089. .59382
/note="L1R1A1 repeat: matches 10. .365 of consensus"
60133. .60174
/note="21 copies 2 mer ca 90% conserved"
60141. .60176
/note="9 copies 4 mer caca 94% conserved"
60574. .60918
/note="M1R2PB repeat: matches 1. .344 of consensus"
60963. .60988
/note="13 copies 2 mer ca 92% conserved"
60989. .61041

```

```

Query March 85.0%; Score 17; DB 9; Length 172064;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3 CAGTCGATATCAGTCGA 19
|||||
169291 CAGTCGATATCAGTCGA 169307

```

```

RESULT 3
AC016760
LOCUS
DEFINITION
Homo sapiens chromosome 13 clone RP11-536M12, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
ACCESSION
AC016760
VERSION
AC016760.4 GI:8568907
KEYWORDS
HTG; HTGS; PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193858)
2 (bases 1 to 193858)
The sequence of Homo sapiens clone
Unpublished
Waterson, R.H.
REFERENCE
Waterson, R.H.
AUTHORS
Waterson, R.H.
TITLE
The sequence of Homo sapiens clone
JOURNAL
Unpublished
AUTHORS
Waterson, R.H.
JOURNAL
Unpublished

```

COMMENT

On Jun 16, 2000 this sequence version replaced gi:6850523.

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0536M12
----- Summary Statistics -----
Sequencing vector: M13: 88%
Chemistry: Dye-terminator Big Dye 1.8% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181257 bases at least Q40
Consensus quality: 185575 bases at least Q30
Consensus quality: 188576 bases at least Q20
Insert size: 184000; agarose-fp
Insert size: 192758; sum-of-contigs
Quality coverage: 4.34 in Q20 bases; sum-of-contigs
----- NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 1629: contig of 1629 bp in length
1630 1729: gap of unknown length
1730 4727: contig of 2998 bp in length
4728 4827: gap of unknown length
4828 8897: contig of 4070 bp in length
8898 8997: gap of unknown length
8998 14918: contig of 5921 bp in length
14919 15018: gap of unknown length
15019 21728: contig of 6710 bp in length
21729 21828: gap of unknown length
21829 36092: gap of 14264 bp in length
36093 36192: gap of unknown length
36193 51210: contig of 14918 bp in length
51211 71759: contig of 20549 bp in length
71760 71860: gap of unknown length
71861 97430: contig of 25570 bp in length
97431 97530: gap of unknown length
97531 122384: contig of 24855 bp in length
122385 122484: gap of unknown length
122485 154483: contig of 31999 bp in length

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FEATURES

* 154484 154583: gap of unknown length

* 154584 193858: contig of 39275 bp in length.

source

1. 193858

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="13"

/clone="RP11-536M12"

misc_feature

1.1629

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4828..8897

/note="assembly_name:Contig9"

8998..14918

/note="assembly_name:Contig10"

clone_end:T7

vector_side:right"

15019..21728

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21829..36092

/note="assembly_name:Contig12"

36193..51110

/note="assembly_name:Contig13"

51211..71759

/note="assembly_name:Contig14"

71860..97429

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97530..122384

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122485..154483

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154584..193858

/note="assembly_name:Contig18"

clone_end:SP6

vector_side:right"

ORIGIN

Query Match 85.0%; Score 17; DB 2; Length 193858;

Best Local Similarity 100.0%; Pred. No. 4.7;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CAGTCGATATCACTGCGA 19

DB 180196 CAGTCGATATCACTGCGA 180212

RESULT 4

AP096709/c 15911 bp DNA linear INV 09-JUN-1999

LOCUS AP096709

DEFINITION Drosophila virilis tyrosyl-tRNA synthetase gene, partial cds; and failed axon connections protein (fax) gene, complete cds.

ACCESSION AP096709

VERSION AF096709.1 GI:4128222

KEYWORDS

SOURCE

ORGANISM

Drosophila virilis

Drosophila virilis

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 15911)

Bedian,V., Jungklaus,C.E., Cardozo,L. and von Kalm,L.

kinase activity and genetic characterization of a growth related antigen of Drosophila

Dev. Genet. 12 (3), 188-195 (1991)

REFERENCE

AUTHORS

JOURNAL

MEDLINE

PUBMED

91330447

1868624

2 (bases 1 to 15911)

Hill,K.K., Bedian,V., Juang,J.L. and Hoffmann,F.M.

Genetic interactions between the Drosophila Abelson (Abi) tyrosine kinase and failed axon connections (fax), a novel protein in axon bundles

JOURNAL

Genetics 141 (2), 595-606 (1995)

MEDLINE

96109606

PUBMED

8647396

3 (bases 1 to 15911)

AUTHORS

Geiger,B.A., Park,C., Rees,H., Frederick,J. and Bedian,V.

TITLE

Direct Submission

JOURNAL

Submitted (02-OCT-1998) Genetics, University of Pennsylvania, 476

CRS, 415 Curie Blvd, Philadelphia, PA 19104, USA

location/Qualifiers

1. 15911

FEATURES

source

1. 15911

/organism="Drosophila virilis"

/mol_type="genomic DNA"

/db_xref="taxon:7244"

/map="72F"

/note="putative chromosome and map positions based on Drosophila melanogaster map positions"

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/product="tyr-tRNA synthetase"

complement(join(<220..285,341..986))

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/product="tyrosyl-tRNA synthetase"

/protein_id="AAD03560.1"

/db_xref="GI:4128224"

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<6683..>14015

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/gene="fax"

/product="failed axon connections protein"

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/product="failed axon connections protein"

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/db_xref="GI:4128223"

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ORIGIN

Query Match 80.0%; Score 16; DB 3; Length 15911;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCCGATATCACTCGAT 20

DB 8933 GTCCGATATCACTCGAT 8918

RESULT 5

AC091300/c 64915 bp DNA linear VRT 16-OCT-2002

LOCUS AC091300

DEFINITION Danio rerio clone 127K3, complete sequence.

ACCESSION AC091300

VERSION AC091300.3 GI:24022405

KEYWORDS

HTG.

SOURCE

ORGANISM

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.